WHAT IS CLAIMED IS:

1 A method comprising:

a) imaging a subject by at least two different modalities of scanning probe microscopy (SPM);

b) using a model of the physical structure of the subject to analyze the images;

c) estimating the values of one or more parameters from the images; and

d) fusing the estimated parameters obtained from the different images.

2. The method of claim 1, wherein parameter fusion is based on the model of the physical structure of the subject.

3. The method of claim 1, further comprising using the fused parameters to characterize the subject.

4. The method of claim 3, further comprising identifying the subject.

5. The method of claim 4, further comprising comparing the fused parameters with parameters determined from known subjects to identify an occurrence of a known subject.

6. The method of claim 1, wherein the SPM imaging includes at least two modalities selected from the group consisting of atomic force microscopy (AFM), scanning tunneling microscopy (STM), lateral force microscopy (LFM), chemical force microscopy (CFM), force modulation imaging, magnetic force microscopy (MFM), high frequency MFM, magnetoresistive sensitivity mapping (MSM), electric force microscopy (EFM), scanning capacitance microscopy (SCM), scanning spreading resistance microscopy (SSRM), tunneling AFM and conductive AFM.

7. The method of claim 1 wherein the subject is a biomolecule.

8. The method of claim 1, wherein the parameters are estimated by level set techniques, PDE (partial differential equation) techniques and/or active surface techniques.

9. The method of claim 8, further comprising embedding the techniques in a probabilistic (Bayesian) estimation framework to account for model uncertainty and instrument noise.

10. The method of claim 1, further comprising classifying the subject by applying vector quantization, support vector machines and/or a statistical classifier to the fused parameters.

11. The method of claim 10, further comprising using known biomolecule structures to generate training sets of data.

12. The method of claim 7, further comprising using known biomolecule structures to obtain ranges of parameters for each type of biomolecule.

13. The method of claim 12, wherein the parameter ranges for known biomolecules are used to constrain the possible values of the estimated parameters.

14. The method of claim 1, wherein the subject is aligned on a surface by molecular combing.

15. A method comprising:

a) analyzing a set of SPM images utilizing a coarse data set to detect locations of potential occurrences of one or more subjects; and

b) reanalyzing the data from the detected locations one or more additional times, with each analysis utilizing a data set that is more refined than the previous analysis.

16. The method of claim 15, wherein a high resolution data set is obtained for each image.

17. The method of claim 15, wherein a low resolution data set is obtained for each image.

18. The method of claim 17, further comprising rescanning the detected locations to obtain a high resolution data set at each location.

19. The method of claim 18, wherein the coarse data set is analyzed while the SPM probe is scanning the location.

20. The method of claim 15, wherein a fused posterior distribution of parameters is analyzed.

21. The method of claim 20, further comprising comparing the fused posterior distribution of parameters with parameter ranges obtained from known subjects to detect locations of potential occurrences of subjects.

22. The method of claim 15, wherein the subjects are biomolecules.

23. The method of claim 22, wherein the subjects are proteins and/or nucleic acids.

24. A structure identification system comprising:

a) a scanning probe microscope with a plurality of imaging modalities;

b) a controller to control the operation of the scanning probe microscope; and

c) a memory to include one or more characterizations of known structures

25. The system of claim 24, wherein the characterizations of known structures represent sets of fused parameters derived from a plurality of known biomolecule structures.

26. The system of claim 25, wherein the characterizations of known structures are used to analyze a set of SPM images.

27. The system of claim 26, wherein the SPM images are obtained by two or more SPM modalities.

28. The system of claim 27, wherein the SPM images are analyzed to identify an occurrence of one or more known structures in a sample.

29. The system of claim 28, wherein the SPM images are analyzed by (i) analyzing a coarse data set to detect locations of potential occurrences of known structures; and (ii) reanalyzing the locations of the potential occurrences one or more additional times, with each analysis utilizing a set of data that is more refined than the set of data utilized in the previous analysis.